

SEQUENCE LISTING

<110> Gao, Zeren
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 Piddington, Christopher S.
 Sheppard, Paul O.
 Shoemaker, Kimberly E.
 Gilbertson, Debra G.
 West, James W.

<120> GROWTH FACTOR HOMOLOG ZVEGF3

<130> 98-60C1

<160> 50

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<211> 1760

<212> DNA

<213> Homo sapiens

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<221> CDS

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cgccgtgagt	gagctctcac	cccagtcagc	caa atg agc ctc ttc	ggg ctt ctc		174
			Met Ser Leu Phe Gly Leu Leu			
			1	5		

ctg ctg aca tct gcc	ctg gcc ggc	cag aga cag ggg	act cag gcg gaa	222
Leu Leu Thr Ser Ala	Leu Ala Gly Gln Arg	Gln Gly Thr Gln Ala	Glu	
10	15	20		

tcc aac ctg agt agt	aaa ttc cag ttt	tcc agc aac aag	gaa cag aac	270
Ser Asn Leu Ser Ser	Lys Phe Gln Phe	Ser Ser Asn Lys	Glu Gln Asn	
25	30	35		

gga gta caa gat cct cag cat gag aga att att act gtg tct act aat 318
 Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn
 40 45 50 55

gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg 366
 Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr
 60 65 70

gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa 414
 Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln
 75 80 85

ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata 462
 Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile
 90 95 100

tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata 510
 Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile
 105 110 115

tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct 558
 Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser
 120 125 130 135

aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct 606
 Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro
 140 145 150

tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc 654
 Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe
 155 160 165

aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg 702
 Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu
 170 175 180

gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt 750
 Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu
 185 190 195

att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta 798
 Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu
 200 205 210 215

tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga 846
 Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg
 220 225 230

aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta 894
 Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu
 235 240 245

tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta 942
 Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu
 250 255 260

aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc 990
 Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg
 265 270 275

tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa 1038
 Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln
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tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg 1086
 Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu
 300 305 310

aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg 1134
 Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val
 315 320 325

gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca 1182
 Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr
 330 335 340

gga gga tag ccgcatcacc accagcagct cttgcccaga gctgtgcagt 1231
 Gly Gly *
 345

gcagtggctg attctattag agaacgtatg cgttatctcc atccttaatc tcagttgttt 1291
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<213> Homo sapiens

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Arg	Gln	Gly	Thr 20	Gln	Ala	Glu	Ser	Asn 25	Leu	Ser	Ser	Lys	Phe 30	Gln	Phe
Ser	Ser	Asn 35	Lys	Glu	Gln	Asn	Gly 40	Val	Gln	Asp	Pro	Gln 45	His	Glu	Arg
Ile 50	Ile	Thr	Val	Ser	Thr	Asn 55	Gly	Ser	Ile	His 60	Ser	Pro	Arg	Phe	Pro
His 65	Thr	Tyr	Pro	Arg	Asn 70	Thr	Val	Leu	Val	Trp 75	Arg	Leu	Val	Ala	Val
Glu	Glu	Asn	Val 85	Trp	Ile	Gln	Leu	Thr	Phe 90	Asp	Glu	Arg	Phe 95	Gly	Leu
Glu	Asp	Pro 100	Glu	Asp	Asp	Ile	Cys 105	Lys	Tyr	Asp	Phe	Val 110	Glu	Val	Glu
Glu	Pro 115	Ser	Asp	Gly	Thr	Ile 120	Leu	Gly	Arg	Trp	Cys 125	Gly	Ser	Gly	Thr
Val 130	Pro	Gly	Lys	Gln	Ile	Ser 135	Lys	Gly	Asn	Gln 140	Ile	Arg	Ile	Arg	Phe
Val 145	Ser	Asp	Glu	Tyr	Phe 150	Pro	Ser	Glu	Pro	Gly 155	Phe	Cys	Ile	His	Tyr
Asn	Ile	Val	Met 165	Pro	Gln	Phe	Thr	Glu	Ala 170	Val	Ser	Pro	Ser 175	Val	Leu
Pro	Pro	Ser	Ala 180	Leu	Pro	Leu	Asp	Leu	Leu 185	Asn	Asn	Ala 190	Ile	Thr	Ala
Phe	Ser	Thr 195	Leu	Glu	Asp	Leu 200	Ile	Arg	Tyr	Leu	Glu 205	Pro	Glu	Arg	Trp
Gln 210	Leu	Asp	Leu	Glu	Asp 215	Leu	Tyr	Arg	Pro	Thr 220	Trp	Gln	Leu	Leu	Gly
Lys 225	Ala	Phe	Val	Phe	Gly 230	Arg	Lys	Ser	Arg	Val 235	Val	Asp	Leu	Asn	Leu

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
 245 250 255
 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
 260 265 270
 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
 275 280 285
 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
 290 295 300
 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
 305 310 315 320
 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
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 Cys Val Cys Arg Gly Ser Thr Gly Gly
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 <223> Xaa is any amino acid

<221> VARIANT
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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30		
Xaa	Xaa	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40						45			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50				55					60					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70				75						80	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			85					90						95		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100				105							110		
Xaa	Cys	Xaa	Cys													
			115													

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<221> VARIANT

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 <223> n = A,T,C or G

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gtncargayc	cncarcayga	rmgnathath	acngtnwsna	cnaayggnws	nathcaywsn	180	
ccnmgnnttyc	cncayacnta	yccnmgnaay	acngtnytn	tntggmgnyt	ngtngcngtn	240	
gargaraayg	tntggathca	rytnacntty	gaygarmgt	tyggnytn	rgayccngar	300	
gaygayatht	gyaartayga	ytygtngar	gtngargarc	cnwsngaygg	nacnathytn	360	
ggnmgntggt	gyggwnsngg	nacngtnccn	ggnaarcara	thwsnaargg	naaycarath	420	
mgnathmgnt	tygtwnsnga	ygartaytty	ccnwsngarc	cnggnttytg	yathcaytay	480	
aayathgtna	tgccncartt	yacngargcn	gtwnsnccnw	sngtnytncc	nccnwsngcn	540	
ytnccnytn	ayytnytnaa	yaaygcna	acngcnttyw	snacnytn	rgayytnath	600	
mgntayytn	arccngarmg	ntggcarytn	gayytn	gargayytn	ayytnaymg	nccnacntgg	660
carytnytn	gnaargcntt	ygtnttygg	mgnaarwsnm	gngtngtn	gayytnaay	yytnaayytn	720
ytnacngarg	argtnmgnyt	ntaywsntgy	acnccnmgna	aytywsngt	nwsnathmg	n	780
gargarytna	armgnacnga	yacnathtty	tggccnggnt	gyytnytn	ngtngayytn	naarmgntgy	840
ggnggnaayt	gygcntgyt	yytncaaya	tgyaaygart	gycartgyt	nccnwsnaar		900
gtnacnaara	artaycayga	rgtnytn	caraytnmg	ncn	aracnggngt	nmgnggnytn	960
cayaarwsny	tnacngaygt	ngcnytn	garayytn	ngtngayytn	artgygaytg	ygtntgymgn	1020
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 <223> n = A,T,C or G

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 mgntgyggng gnaaytg 17

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<210> 10
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<210> 11

<211> 17

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ntnddnccnn sntgybt

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<210> 12

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<222> (1)...(17)

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<210> 13

<211> 17

<212> DNA

<213> Artificial Sequence

<223> Oligonucleotide primer

caygargart gygaytg

17

<211> 17

<213> Artificial Sequence

<223> Oligonucleotide primer

 $\langle 222 \rangle \quad (1) \dots (17)$

<223> n = A,T,C or G

caynnnnvnt gyvvntg

17

<211> 17

<213> Artificial Sequence

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 $\langle 222 \rangle \quad (1) \dots (17)$

<223> n = A,T,C or G

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17

<211> 17

<213> Artificial Sequence

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<223> Oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

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<210> 17

<211> 17

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<223> Oligonucleotide primer

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<222> (1)...(17)

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<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer

<221> misc_feature

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<223> n = A,T,C or G

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dhnkynmkng knndrca

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<210> 19

<211> 17

<212> DNA

<213> Artificial Sequence

<223> Oligonucleotide primer

<400> 19

<211> 17

<213> Artificial Sequence

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 $\langle 222 \rangle \quad (1) \dots (17)$

<223> n = A,T,C or G

<400> 21

<211> 17

<213> Artificial Sequence

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<223> n = A,T,C or G

<400> 22

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<210> 23

<211> 17

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<222> (1)...(17)

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<210> 24

<211> 17

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<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 24

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<210> 25

<211> 20

<212> DNA

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ggaggtctat ataagcagag c	21
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<211> 25

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<223> Oligonucleotide primer

<400> 31

<211> 27

<213> Artificial Sequence

<223> Oligonucleotide primer

<400> 32

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<213> Artificial Sequence

$\langle 220 \rangle$

<223> Oligonucleotide primer

<400> 33

cttttgctag cctcaaccct gactatc

27

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<212> DNA

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<223> Oligonucleotide primer ZC20,181

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<212> DNA

<213> Homo sapiens

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<221> CDS

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<400> 36

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cagggcgagc gcaggcggcg agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac 180

ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc 237

Met His Arg Leu

atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac	285
Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp	
5 10 15 20	
act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc	333
Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala	
25 30 35	
aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga	381
Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg	
40 45 50	
gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga	429
Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg	
55 60 65	
ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac	477
Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His	
70 75 80	
tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga	525
Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly	
85 90 95 100	
tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt	573
Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val	
105 110 115	
gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga	621
Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly	
120 125 130	
cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa	669
His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys	
135 140 145	
atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag	717
Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys	
150 155 160	

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
 345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg agggtagat 1398
 aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
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<210> 37

<211> 370

<212> PRT

<213> Homo sapiens

<400> 37

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 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
 35 40 45
 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
 50 55 60
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65 70 75 80
 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
 85 90 95
 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
 115 120 125

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 130 135 140
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
 180 185 190
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
 195 200 205
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 225 230 235 240
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 275 280 285
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

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<220>
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<220>
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<400> 40
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<210> 41
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<220>
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<400> 41
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<210> 42
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<220>
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 <222> (1049)...(2086)

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ctccgagccg	cccaagctct	cccggcttcc	cgcagcactt	cgccggtacc	cgagggaact	420
tcggtggcca	ccgactgcag	caaggaggag	gtccgcggt	ggatccgggc	cagtcccag	480
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ctccccccag	gtgggggttg	ggcgccgcct	gccgccccga	tcagcagctt	tgtcattgat	600
cccaaggtgc	tcgcctcgct	gccgacctgg	cttccagtct	ggcttggcgg	gaccccgagt	660
cctcgcctgt	gtcctgtccc	ccaaactgac	aggtgctccc	tgcgagtcgc	cacgactcat	720
cgccgctccc	ccgcgtcccc	accctttctt	tcctccctcg	cctaccccca	ccccccgcac	780
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agcgcagcct	ttccccggct	gggctgagcc	ttggagtcgt	cgcttcccca	gtgcccgccg	1020
cgaqtgaqcc	ctcgcctccag	tcagccaa	atg ctc ctc ctc ggc ctc ctc ctg			1072

1

5

10.

15

20

25

30

35

40

45

50

55

60

65

70

75

80

85

aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc 1360
 Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys
 90 95 100

aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta 1408
 Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu
 105 110 115 120

gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa 1456
 Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys
 125 130 135

gga aat cat atc agg ata aga ttt gta tct gat gag tat ttt cca tct 1504
 Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser
 140 145 150

gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca 1552
 Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr
 155 160 165

gaa acc acg agt cct tcg gtg ttg ccc cct tca tct ttg tca ttg gac 1600
 Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp
 170 175 180

ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att 1648
 Leu Leu Asn Asn Ala Val Thr Ala Phe Ser Thr Leu Glu Glu Leu Ile
 185 190 195 200

cgg tac cta gag cca gat cga tgg cag gtg gac ttg gac agc ctc tac 1696
 Arg Tyr Leu Glu Pro Asp Arg Trp Gln Val Asp Leu Asp Ser Leu Tyr
 205 210 215

aag cca aca tgg cag ctt ttg ggc aag gct ttc ctg tat ggg aaa aaa 1744
 Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys
 220 225 230

agc aaa gtg gtg aat ctg aat ctc ctc aag gaa gag gta aaa ctc tac 1792
 Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr
 235 240 245

agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag 1840
 Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys
 250 255 260


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<212> PRT

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 20          25          30
Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
 35          40          45
Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
 50          55          60
His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
 65          70          75          80
Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
 85          90          95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
100          105          110
Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
115          120          125
Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
130          135          140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145          150          155          160
Ser Ile Ile Met Pro Gln Val Thr Glu Thr Thr Ser Pro Ser Val Leu
165          170          175
Pro Pro Ser Ser Leu Ser Leu Asp Leu Leu Asn Asn Ala Val Thr Ala
180          185          190
Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
195          200          205
Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly
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<400> 45
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<213> Artificial Sequence

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<223> oligonucleotide primer ZC19,351

<400> 47

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<210> 48

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC19,352

<400> 48

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<210> 49

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC19,371

<400> 49

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<223> Fused DNA

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